Package ‘meshes’

January 12, 2024

Title MeSH Enrichment and Semantic analyses

Version 1.28.0

Description MeSH (Medical Subject Headings) is the NLM controlled vocabulary used to manually index articles for MEDLINE/PubMed. MeSH terms were associated by Entrez Gene ID by three methods, gendoo, gene2pubmed and RBBH. This association is fundamental for enrichment and semantic analyses. meshes supports enrichment analysis (over-representation and gene set enrichment analysis) of gene list or whole expression profile. The semantic comparisons of MeSH terms provide quantitative ways to compute similarities between genes and gene groups. meshes implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively and supports more than 70 species.

Depends R (>= 4.1.0)

Imports AnnotationDbi, DOSE, enrichplot, GOSeqSim, methods, utils, AnnotationHub, MeSHDbi, yulab.utils

Suggests knitr, rmarkdown, prettydoc

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0


BugReports https://github.com/GuangchuangYu/meshes/issues

biocViews Annotation, Clustering, MultipleComparison, Software

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

git_url https://git.bioconductor.org/packages/meshes

git_branch RELEASE_3_18

Date 2023-10-24

git_last_commit 227153b

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18
Description

MeSH term enrichment analysis

Usage

enrichMeSH(
  gene,
  MeSHDb,
  database = "gendoo",
  category = "C",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  qvalueCutoff = 0.2,
  minGSSize = 10,
  maxGSSize = 500,
  meshdbVersion = NULL
)

Arguments

gene a vector of entrez gene id
MeSHDb MeSHDb
database one of 'gendoo', 'gene2pubmed' or 'RBBH'
geneSim

<table>
<thead>
<tr>
<th>Category</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>pvalueCutoff</td>
<td>Cutoff value of pvalue.</td>
</tr>
<tr>
<td>pAdjustMethod</td>
<td>one of &quot;holm&quot;, &quot;hochberg&quot;, &quot;hommel&quot;, &quot;bonferroni&quot;, &quot;BH&quot;, &quot;BY&quot;, &quot;fdr&quot;, &quot;none&quot;</td>
</tr>
<tr>
<td>universe</td>
<td>background genes</td>
</tr>
<tr>
<td>qvalueCutoff</td>
<td>qvalue cutoff</td>
</tr>
<tr>
<td>minGSSize</td>
<td>minimal size of genes annotated by Ontology term for testing.</td>
</tr>
<tr>
<td>maxGSSize</td>
<td>maximal size of genes annotated for testing</td>
</tr>
<tr>
<td>meshdbVersion</td>
<td>version of MeSH.db. If NULL (the default), use the latest version.</td>
</tr>
</tbody>
</table>

Value

An enrichResult instance.

Author(s)

Guangchuang Yu

See Also

class?enrichResult

Examples

```r
## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichMeSH(de, MeSHDb = db, database='gendo', category = 'C')
```

```r
## End(Not run)
```

Description

semantic similarity between two gene vector

Usage

geneSim(geneID1, geneID2 = NULL, measure = "Wang", combine = "BMA", semData)
Arguments

- `geneID1` gene ID vector
- `geneID2` gene ID vector
- `measure` one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"
- `combine` One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple DO terms associated with gene/protein.
- `semData` gene annotation data for semantic measurement

Value

score matrix

Author(s)

Guangchuang Yu

Examples

```r
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDbi::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category="A", computeIC=T, database="gendoo")
data(hsamd)
geneSim("241", "251", semData=hsamd, measure="Wang", combine="BMA")
```

Description

Gene Set Enrichment Analysis of MeSH

Usage

```r
gseMeSH(  
geneList,  
MeSHDb,  
database = "gendoo",  
category = "C",  
exponent = 1,  
minGSSize = 10,  
maxGSSize = 500,  
eps = 1e-10,  
pvalueCutoff = 0.05,
)```
gseMeSH

pAdjustMethod = "BH",
verbose = TRUE,
seed = FALSE,
by = "fgsea",
meshdbVersion = NULL,
...
)

Arguments
geneList          order ranked geneList
MeSHDb            MeSHDb
database          one of ‘gendoo’, ‘gene2pubmed’ or ‘RBBH’
exponent          weight of each step
minGSSize         minimal size of each geneSet for analyzing
maxGSSize         maximal size of genes annotated for testing
eps               This parameter sets the boundary for calculating the p value.
pvalueCutoff      pvalue Cutoff
pAdjustMethod     pvalue adjustment method
verbose           print message or not
seed              logical
by                one of ‘fgsea’ or ‘DOSE’
meshdbVersion     version of MeSH.db. If NULL (the default), use the latest version.
...                other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

Examples

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
y <- gseMeSH(geneList, MeSHDb = db, database = 'gene2pubmed', category = "G")

## End(Not run)
Description

construct annoData for semantic measurement

Usage

meshdata(MeSHDb = NULL, database, category, computeIC = FALSE)

Arguments

- **MeSHDb**: MeSHDb package
- **database**: one of supported database
- **category**: one of supported category
- **computeIC**: logical value

Value

a GOSemSimDATA object

Author(s)

Guangchuang Yu

Examples

```r
## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDb::MeSHDb(filepath_hsa)
hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")
## End(Not run)
```
meshSim

Description
semantic similarity between two MeSH term vectors

Usage
meshSim(meshID1, meshID2, measure = "Wang", semData)

Arguments
meshID1 MeSH term vector
meshID2 MeSH term vector
measure one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"
semData annotation data for semantic measurement, output by meshdata function

Value
score matrix

Author(s)
Guangchuang Yu https://guangchuangyu.github.io

Examples
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDb::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")
data(hsamd)
meshSim("D000009", "D009130", semData=hsamd, measure="Resnik")

mesh_term_table

Description
These datasets are used in meshes

DATA Sets
Objects exported from other packages

Description
These objects are imported from other packages. Follow the links below to see their documentation.

**DOSE**  geneID, geneInCategory
**enrichplot**  cnetplot, dotplot, emapplot, gseaplot, heatplot, ridgeplot
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